

1 SEQUENCE LISTING

<110> Moore, et al.

<120> Human FK506 Binding Proteins

<130> PF392

<140> Unassigned

<141> 1999-01-06

<150> 60/070,875

<151> 1998-01-09

<160> 8

<170> PatentIn Ver. 2.0

<210> 1

<211> 1234

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (61)..(1008)

<400> 1

ggaggttggt ggcgactccc tcgctcgccc tcaactgccg cggtcccaac tccaggcacc 60

atg	ttc	ccc	gcg	ggc	ccc	ccc	agc	cac	agc	ctc	ctc	cgg	ctc	ccc	ctg	108
Met	Phe	Pro	Ala	Gly	Pro	Pro	Ser	His	Ser	Leu	Leu	Arg	Leu	Pro	Leu	
1				5					10					15		

ctg	cag	ttg	ctg	cta	ctg	gtg	gtg	cag	gcc	gtg	ggg	agg	ggg	ctg	ggc	156
Leu	Gln	Leu	Leu	Leu	Val	Val	Gln	Ala	Val	Gly	Arg	Gly	Leu	Gly		
			20				25					30				

cgc	gcc	agc	cgc	gcc	ggg	ggc	ccc	ctg	gaa	gat	gtg	gtc	atc	gag	agg	204
Arg	Ala	Ser	Pro	Ala	Gly	Gly	Pro	Leu	Glu	Asp	Val	Val	Ile	Glu	Arg	
		35					40					45				

tac	cac	atc	ccc	agg	gcc	tgt	ccc	cgg	gaa	gtg	cag	atg	ggg	gat	ttt	252
Tyr	His	Ile	Pro	Arg	Ala	Cys	Pro	Arg	Glu	Val	Gln	Met	Gly	Asp	Phe	
	50					55					60					

gtg	cgc	tac	cac	tac	aac	ggc	act	ttt	gaa	gat	ggc	aag	aag	ttt	gat	300
Val	Arg	Tyr	His	Tyr	Asn	Gly	Thr	Phe	Glu	Asp	Gly	Lys	Lys	Phe	Asp	
65					70					75				80		

tca	agc	tat	gat	cgc	aac	acc	ttg	gtg	gcc	atc	gtg	gtg	ggt	gtg	ggg	348
Ser	Ser	Tyr	Asp	Arg	Asn	Thr	Leu	Val	Ala	Ile	Val	Val	Gly	Val	Gly	
				85					90					95		

cgc	ctc	atc	act	ggc	atg	gac	cga	ggc	ctc	atg	ggc	atg	tgt	gtc	aac	396
Arg	Leu	Ile	Thr	Gly	Met	Asp	Arg	Gly	Leu	Met	Gly	Met	Cys	Val	Asn	
			100					105					110			

gag	cgg	cga	cgc	ctc	att	gtg	cct	ccc	cac	ctg	ggc	tat	ggg	agc	atc	444
Glu	Arg	Arg	Arg	Leu	Ile	Val	Pro	Pro	His	Leu	Gly	Tyr	Gly	Ser	Ile	
			115				120					125				

09225502 " 010699

ggc ctg gcg ggg ctc att cca ccg gat gcc acc ctc tac ttc gat gtg 492
 Gly Leu Ala Gly Leu Ile Pro Pro Asp Ala Thr Leu Tyr Phe Asp Val
 130 135 140
 gtt ctg ctg gat gtg tgg aac aag gaa gac acc gtg cag gtg agc aca 540
 Val Leu Leu Asp Val Trp Asn Lys Glu Asp Thr Val Gln Val Ser Thr
 145 150 155 160
 ttg ctg cgc ccg ccc cac tgc ccc cgc atg gtc cag gac ggc gac ttt 588
 Leu Leu Arg Pro Pro His Cys Pro Arg Met Val Gln Asp Gly Asp Phe
 165 170 175
 gtc cgc tac cac tac aat ggc acc ctg ctg gac ggc acc ttc ttc gac 636
 Val Arg Tyr His Tyr Asn Gly Thr Leu Leu Asp Gly Thr Ser Phe Asp
 180 185 190
 acc agc tac agt aag ggc ggc act tat gac acc tac gtc ggc tct ggt 684
 Thr Ser Tyr Ser Lys Gly Gly Thr Tyr Asp Thr Tyr Val Gly Ser Gly
 195 200 205
 tgg ctg atc aag ggc atg gac cag ggg ctg ctg ggc atg tgt cct gga 732
 Trp Leu Ile Lys Gly Met Asp Gln Gly Leu Leu Gly Met Cys Pro Gly
 210 215 220
 cag aga agg aag att atc atc cct cca ttc ctg gcc tat ggc gag aaa 780
 Gln Arg Arg Lys Ile Ile Ile Pro Pro Phe Leu Ala Tyr Gly Glu Lys
 225 230 235 240
 ggc tat ggt gag ggt ggg caa gga cac aag ggc aaa ttc cgc aga aga 828
 Gly Tyr Gly Glu Gly Gly Gln Gly His Lys Gly Lys Phe Arg Arg Arg
 245 250 255
 ggg aaa aac cag gcc tcc aca tac agt tgc tca ggt tgt ata ctg cac 876
 Gly Lys Asn Gln Ala Ser Thr Tyr Ser Cys Ser Gly Cys Ile Leu His
 260 265 270
 gag ggc atc caa cca agg act caa ggt ggg atg aaa tct acc ctt ggt 924
 Glu Gly Ile Gln Pro Arg Thr Gln Gly Gly Met Lys Ser Thr Leu Gly
 275 280 285
 gct act aag aag ggg tgc ttt ggc cgg gcg tgg tgg ctc acg ctt gta 972
 Ala Thr Lys Lys Gly Cys Phe Gly Arg Ala Trp Trp Leu Thr Leu Val
 290 295 300
 atc cca gca ctt tgg gaa gcc aag gcg gga gga tca cgaggtccag 1018
 Ile Pro Ala Leu Trp Glu Ala Lys Ala Gly Gly Ser
 305 310 315
 gagatcgaga ccacggtgaa acccgcgtctc tactaaaaat acaaaaaaat tagccgggcg 1078
 tgggtgggggc gcctgtagt ccagctactc ggagaggctg aggcaggaaa atgacgtgaa 1138
 cccgggaggc ggagcttgca gtgagccgag atcttgccac tgcactccag cctgggtgac 1198
 agagcgagac tctgtctcaa aaaaaaaaaa aaaaaa 1234

<210> 2
 <211> 316
 <212> PRT
 <213> Homo sapiens

00225702 "010699

<400> 2

Met Phe Pro Ala Gly Pro Pro Ser His Ser Leu Leu Arg Leu Pro Leu
 1 5 10 15
 Leu Gln Leu Leu Leu Leu Val Val Gln Ala Val Gly Arg Gly Leu Gly
 20 25 30
 Arg Ala Ser Pro Ala Gly Gly Pro Leu Glu Asp Val Val Ile Glu Arg
 35 40 45
 Tyr His Ile Pro Arg Ala Cys Pro Arg Glu Val Gln Met Gly Asp Phe
 50 55 60
 Val Arg Tyr His Tyr Asn Gly Thr Phe Glu Asp Gly Lys Lys Phe Asp
 65 70 75 80
 Ser Ser Tyr Asp Arg Asn Thr Leu Val Ala Ile Val Val Gly Val Gly
 85 90 95
 Arg Leu Ile Thr Gly Met Asp Arg Gly Leu Met Gly Met Cys Val Asn
 100 105 110
 Glu Arg Arg Arg Leu Ile Val Pro Pro His Leu Gly Tyr Gly Ser Ile
 115 120 125
 Gly Leu Ala Gly Leu Ile Pro Pro Asp Ala Thr Leu Tyr Phe Asp Val
 130 135 140
 Val Leu Leu Asp Val Trp Asn Lys Glu Asp Thr Val Gln Val Ser Thr
 145 150 155 160
 Leu Leu Arg Pro Pro His Cys Pro Arg Met Val Gln Asp Gly Asp Phe
 165 170 175
 Val Arg Tyr His Tyr Asn Gly Thr Leu Leu Asp Gly Thr Ser Phe Asp
 180 185 190
 Thr Ser Tyr Ser Lys Gly Gly Thr Tyr Asp Thr Tyr Val Gly Ser Gly
 195 200 205
 Trp Leu Ile Lys Gly Met Asp Gln Gly Leu Leu Gly Met Cys Pro Gly
 210 215 220
 Gln Arg Arg Lys Ile Ile Ile Pro Pro Phe Leu Ala Tyr Gly Glu Lys
 225 230 235 240
 Gly Tyr Gly Glu Gly Gly Gln Gly His Lys Gly Lys Phe Arg Arg Arg
 245 250 255
 Gly Lys Asn Gln Ala Ser Thr Tyr Ser Cys Ser Gly Cys Ile Leu His
 260 265 270
 Glu Gly Ile Gln Pro Arg Thr Gln Gly Gly Met Lys Ser Thr Leu Gly
 275 280 285
 Ala Thr Lys Lys Gly Cys Phe Gly Arg Ala Trp Trp Leu Thr Leu Val
 290 295 300
 Ile Pro Ala Leu Trp Glu Ala Lys Ala Gly Gly Ser
 305 310 315

09225500-01069

<400>	3
c ttc gat gtg gtt ctg ctg gat gtg tgg aac aag gaa gac acc gtg cag	49
Phe Asp Val Val Leu Leu Asp Val Trp Asn Lys Glu Asp Thr Val Gln	
1 5 10 15	
gtg agc aca ttg ctg cgc ccg ccc cac tgc ccc cgc atg gtc cag gac	97
Val Ser Thr Leu Leu Arg Pro Pro His Cys Pro Arg Met Val Gln Asp	
20 25 30	
ggc gac ttt gtc cgc tac cac tac aat ggc acc ctg ctg gac ggc acc	145
Gly Asp Phe Val Arg Tyr His Tyr Asn Gly Thr Leu Leu Asp Gly Thr	
35 40 45	
tcc ttc gac acc agc tac agt aag ggc ggc act tat gac acc tac gtc	193
Ser Phe Asp Thr Ser Tyr Ser Lys Gly Gly Thr Tyr Asp Thr Tyr Val	
50 55 60	
ggc tct ggt tgg ctg atc aag ggc atg gac cag ggc ctg ctg ggc atg	241
Gly Ser Gly Trp Leu Ile Lys Gly Met Asp Gln Gly Leu Leu Gly Met	
65 70 75 80	
tgt cct gga gag aga agg aag att atc atc cct cca ttc ctg gcc tat	289
Cys Pro Gly Glu Arg Arg Lys Ile Ile Ile Pro Pro Phe Leu Ala Tyr	
85 90 95	
ggc gag aaa ggc tat ggg aca gtg atc ccc cca cag gcc tcg ctg gtc	337
Gly Glu Lys Gly Tyr Gly Thr Val Ile Pro Pro Gln Ala Ser Leu Val	
100 105 110	
ttt cac gtc ctc ctg att gac gtg cac aac ccg aag gac gct gtc cag	385
Phe His Val Leu Leu Ile Asp Val His Asn Pro Lys Asp Ala Val Gln	
115 120 125	
cta gag acg ctg gag ctc coc ccc ggc tgt gtc cgc aga gcc ggg gcc	433
Leu Glu Thr Leu Glu Leu Pro Pro Gly Cys Val Arg Arg Ala Gly Ala	
130 135 140	
ggg gac ttc atg cgc tac cac tac aat ggc tcc ttg atg gac ggc acc	481
Gly Asp Phe Met Arg Tyr His Tyr Asn Gly Ser Leu Met Asp Gly Thr	
145 150 155 160	
ctc ttc gat tcc agc tac tcc cac aac cac acc tac aat acc tat atc	529
Leu Phe Asp Ser Ser Tyr Ser His Asn His Thr Tyr Asn Thr Tyr Ile	
165 170 175	
ggg cag ggt tac atc atc ccc ggg atg gac cag ggc ctg cag ggt gcc	577
Gly Gln Gly Tyr Ile Ile Pro Gly Met Asp Gln Gly Leu Gln Gly Ala	
180 185 190	
tgc atg ggc gaa cgc cgg aga att acc atc ccc ccg cac ctc gcc tat	625
Cys Met Gly Glu Arg Arg Arg Ile Thr Ile Pro Pro His Leu Ala Tyr	
195 200 205	

ggg	gag	aat	gga	act	gga	gac	aag	atc	cct	ggc	tct	gcc	gtg	cta	atc	673
Gly	Glu	Asn	Gly	Thr	Gly	Asp	Lys	Ile	Pro	Gly	Ser	Ala	Val	Leu	Ile	
210					215					220						
ttc	aac	gtc	cat	gtc	att	gac	ttc	cac	aac	cct	gcg	gat	gtg	gtg	gaa	721
Phe	Asn	Val	His	Val	Ile	Asp	Phe	His	Asn	Pro	Ala	Asp	Val	Val	Glu	
225					230					235					240	
atc	agg	aca	ctg	tcc	cgg	cca	tct	gag	acc	tgc	aat	gag	acc	acc	aag	769
Ile	Arg	Thr	Leu	Ser	Arg	Pro	Ser	Glu	Thr	Cys	Asn	Glu	Thr	Thr	Lys	
				245					250					255		
ctt	ggg	gac	ttt	gtt	cga	tac	cat	tac	aac	tgt	tct	ttg	ctg	gac	ggc	817
Leu	Gly	Asp	Phe	Val	Arg	Tyr	His	Tyr	Asn	Cys	Ser	Leu	Leu	Asp	Gly	
			260					265					270			
acc	cag	ctg	ttc	acc	tcg	cat	gac	tac	ggg	gcc	ccc	cag	gag	gcg	act	865
Thr	Gln		Phe	Thr	Ser	His	Asp	Tyr	Gly	Ala	Pro	Gln	Glu	Ala	Thr	
	275						280					285				
ctc	ggg	gcc	aac	aag	gtg	atc	gaa	ggc	ctg	gac	acg	ggc	ctg	cag	ggc	913
Leu	Gly	Ala	Asn	Lys	Val	Ile	Glu	Gly	Leu	Asp	Thr	Gly	Leu	Gln	Gly	
	290					295					300					
atg	tgt	gtg	gga	gag	agg	cgg	cag	ctc	atc	gtg	ccc	ccg	cac	ctg	gcc	961
Met	Cys	Val	Gly	Glu	Arg	Arg	Gln	Leu	Ile	Val	Pro	Pro	His	Leu	Ala	
305					310					315					320	
cac	ggg	gag	agt	gga	gcc	cgg	gga	gtc	cca	ggc	agt	gct	gtg	ctg	ctg	1009
His	Gly	Glu	Ser	Gly	Ala	Arg	Gly	Val	Pro	Gly	Ser	Ala	Val	Leu	Leu	
				325					330					335		
ttt	gag	gtg	gag	ctg	gtg	tcc	cgg	gag	gat	ggg	ctg	ccc	aca	ggc	tac	1057
Phe	Glu	Val	Glu	Leu	Val	Ser	Arg	Glu	Asp	Gly	Leu	Pro	Thr	Gly	Tyr	
			340					345					350			
ctg	ttt	gtg	tgg	cac	aag	gac	cct	cct	gcc	aac	ctg	ttt	gaa	gac	ata	1105
Leu	Phe	Val	Trp	His	Lys	Asp	Pro	Pro	Ala	Asn	Leu	Phe	Glu	Asp	Ile	
			355				360					365				
gac	ctc	aac	aag	gat	ggc	gag	gtc	cct	ccg	gag	gag	ttc	tcc	acc	ttc	1153
Asp	Leu	Asn	Lys	Asp	Gly	Glu	Val	Pro	Pro	Glu	Glu	Phe	Ser	Thr	Phe	
	370					375					380					
atc	aag	gct	caa	gtg	agt	gag	ggc	aaa	gga	cgc	ctc	atg	cct	ggg	cag	1201
Ile	Lys	Ala	Gln	Val	Ser	Glu	Gly	Lys	Gly	Arg	Leu	Met	Pro	Gly	Gln	
385					390					395					400	
gac	cct	gag	aaa	acc	ata	gga	gac	atg	ttc	cag	aac	cag	gac	cgc	aac	1249
Asp	Pro	Glu	Lys	Thr	Ile	Gly	Asp	Met	Phe	Gln	Asn	Gln	Asp	Arg	Asn	
				405					410					415		
cag	gac	ggc	aag	atc	aca	gtc	gac	gag								

```
<210> 4
<211> 441
<212> PRT
<213> Homo sapiens
```

Phe Asp Val Val Leu Leu Asp Val Trp / Asn Lys Glu Asp Thr Val Gln
1 5 10 15

Val Ser Thr Leu Leu Arg Pro Pro His Cys Pro Arg Met Val Gln Asp
20 25 30

Gly Asp Phe Val Arg Tyr His Tyr Asn Gly Thr Leu Leu Asp Gly Thr
35 40 45

Ser Phe Asp Thr Ser Tyr Ser Lys Gly Gly Thr Tyr Asp Thr Tyr Val
50 55 60

Gly Ser Gly Trp Leu Ile Lys Gly Met Asp Gln Gly Leu Leu Gly Met
65 70 75 80

Cys Pro Gly Glu Arg Arg Lys Ile Ile Ile Pro Pro Phe Leu Ala Tyr
85 90 95

Gly Glu Lys Gly Tyr Gly Thr Val Ile Pro Pro Gln Ala Ser Leu Val
100 105 110

Phe His Val Leu ~~Leu~~ Ile Asp Val His Asn Pro Lys Asp Ala Val Gln
115 120 125

Leu Glu Thr Leu Glu Leu Pro Pro Gly Cys Val Arg Arg Ala Gly Ala
130 135 140

Gly Asp Phe Met Arg Tyr His Tyr Asn Gly Ser Leu Met Asp Gly Thr
145 150 155 160

```
<210> 5
<211> 3451
<212> DNA
<213> Homo sapiens
<220>
```

<221> CDS
<222> (130)..(1752)

<220>
<221> misc_feature
<222> (1124)
<223> n equals a, t, g, or c

<220>
<221> misc_feature
<222> (2061)
<223> n equals a, t, g, or c

<220>
<221> misc_feature
<222> (2111)
<223> n equals a, t, g, or c

<220>
<221> misc_feature
<222> (2171)
<223> n equals a, t, g, or c

<220>
<221> misc_feature
<222> (2411)
<223> n equals a, t, g, or c

<220>
<221> misc_feature
<222> (2449)
<223> n equals a, t, g, or c

<220>
<221> misc_feature
<222> (2451)..(2452)
<223> n equals a, t, g, or c

<220>
<221> misc_feature
<222> (2470)
<223> n equals a, t, g, or c

<220>
<221> misc_feature
<222> (2475)
<223> n equals a, t, g, or c

<220>
<221> misc_feature
<222> (2477)
<223> n equals a, t, g, or c

<220>
<221> misc_feature
<222> (2485)
<223> n equals a, t, g, or c

<220>
<221> misc_feature
<222> (2520)
<223> n equals a, t, g, or c

00225500-010699

<220>
 <221> misc_feature
 <222> (2529)
 <223> n equals a, t, g, or c

<220>
 <221> misc_feature
 <222> (2570)
 <223> n equals a, t, g, or c

<220>
 <221> misc_feature
 <222> (2581)
 <223> n equals a, t, g, or c

<220>
 <221> misc_feature
 <222> (2589)
 <223> n equals a, t, g, or c

<220>
 <221> misc_feature
 <222> (2600)
 <223> n equals a, t, g, or c

<220>
 <221> misc_feature
 <222> (2602)
 <223> n equals a, t, g, or c

<220>
 <221> misc_feature
 <222> (2604)
 <223> n equals a, t, g, or c

<220>
 <221> misc_feature
 <222> (2606)
 <223> n equals a, t, g, or c

<220>
 <221> misc_feature
 <222> (2611)
 <223> n equals a, t, g, or c

<220>
 <221> misc_feature
 <222> (2613)
 <223> n equals a, t, g, or c

<400> 5
 gcgtccgcgg ctgcagcccc ggtagggcca ggagaccggt tccacgtttg caaacgcagc 60
 cgaacgcccc ggccgaccgg tgccgcccga gcgcgcgcgt gcgtccgcgc cactttctc 120
 gccgccccg atg gcg ttc cgg ggc tgg agg ccc ccg ccg cca ccg ctg ctc 171
 Met Ala Phe Arg Gly Trp Arg Pro Pro Pro Pro Leu Leu
 1 5 10

ctg ctg ctg ctc tgg gtg acc ggg cag gca gcg ccc gtg gcg ggc ctg 219
 Leu Leu Leu Leu Trp Val Thr Gly Gln Ala Ala Pro Val Ala Gly Leu

09225502-010699

15	20	25	30	
ggc tcc gac gcg gag ctg cag atc gag cgg cgc ttc gtg ccc gac gag	267			
Gly Ser Asp Ala Glu Leu Gln Ile Glu Arg Arg Phe Val Pro Asp Glu				
35 40 45				
tgc ccg cgc acc gtg cgc agc ggc gac ttc gtg cgc tac cac tac gtg	315			
Cys Pro Arg Thr Val Arg Ser Gly Asp Phe Val Arg Tyr His Tyr Val				
50 55 60				
ggg acg ttc ccc gac ggc cag aag ttc gac tcc agc tat gac aga gac	363			
Gly Thr Phe Pro Asp Gly Gln Lys Phe Asp Ser Ser Tyr Asp Arg Asp				
65 70 75				
tcc act ttc aat gtg ttt gtg gga aaa gga cag ctg atc aca ggg atg	411			
Ser Thr Phe Asn Val Phe Val Gly Lys Gly Gln Leu Ile Thr Gly Met				
80 85 90				
gac cag gct ctt gtt ggg atg tgc gta aac gag aga cct ttc gtg aag	459			
Asp Gln Ala Leu Val Gly Met Cys Val Asn Glu Arg Arg Phe Val Lys				
95 100 105 110				
att ccc cca aag ctt gcc tac gga aat gaa aga gtt tct ggt gtg atc	507			
Ile Pro Pro Lys Leu Ala Tyr Gly Asn Glu Arg Val Ser Gly Val Ile				
115 120 125				
ccc ccc aat tca gtg ctt cat ttt gat gta ctt ctg atg gat att tgg	555			
Pro Pro Asn Ser Val Leu His Phe Asp Val Leu Leu Met Asp Ile Trp				
130 135 140				
aat tct gaa gac cag gtt cag att cac acc tat ttc aag ccc ccg agt	603			
Asn Ser Glu Asp Gln Val Gln Ile His Thr Tyr Phe Lys Pro Pro Ser				
145 150 155				
tgc cct cgg acc atc cag gtg tct gat ttt gtg agg tac cac tac aac	651			
Cys Pro Arg Thr Ile Gln Val Ser Asp Phe Val Arg Tyr His Tyr Asn				
160 165 170				
ggg acg ttc ctg gac gga act ctg ttt gat tgc agt cac aat cgc atg	699			
Gly Thr Phe Leu Asp Gly Thr Leu Phe Asp Ser Ser His Asn Arg Met				
175 180 185 190				
aaa aca tat gac acg tat gtg gga att ggc tgg ctg att cct gga atg	747			
Lys Thr Tyr Asp Thr Val Gly Ile Gly Trp Leu Ile Pro Gly Met				
195 200 205				
gat aaa ggg ctg ctg ggg atg tgt gtg ggt gag aag cgc atc atc acc	795			
Asp Lys Gly Leu Leu Gly Met Cys Val Gly Glu Lys Arg Ile Ile Thr				
210 215 220				
att cct cct ttt ctg gcc tat gga gag gat gga gat ggg aaa gac att	843			
Ile Pro Pro Phe Leu Ala Tyr Gly Glu Asp Gly Asp Gly Lys Asp Ile				
225 230 235				
ccc ggt cag gca tct ctg gtg ttt gat gtt gca tta ttg gac ctc cat	891			
Pro Gly Gln Ala Ser Leu Val Phe Asp Val Ala Leu Leu Asp Leu His				
240 245 250				
aac ccc aag gac agc att tcc att gag aac aag gta gta cct gaa aac	939			
Asn Pro Lys Asp Ser Ile Ser Ile Glu Asn Lys Val Val Pro Glu Asn				
255 260 265 270				

09225502 "010699

tgt gag cgg ata agt caa agt ggg gac ttt ctc acg tat cat tac aat 987
 Cys Glu Arg Ile Ser Gln Ser Gly Asp Phe Leu Thr Tyr His Tyr Asn 285
 275 280

ggc acg ctt ctg gat ggc acc ctc ttt gat tcc agc tac tct cgg aac 1035
 Gly Thr Leu Leu Asp Gly Thr Leu Phe Asp Ser Ser Tyr Ser Arg Asn 300
 290 295

cgc acg ttt gac acg tac att ggg cag ggc tac gtg att cct ggg atg 1083
 Arg Thr Phe Asp Thr Tyr Ile Gly Gln Gly Tyr Val Ile Pro Gly Met 315
 305 310

gat gaa ggt cta ctt ggt gtt tgc att gga gaa aag cga ang att gtg 1131
 Asp Glu Gly Leu Leu Gly Val Cys Ile Gly Glu Lys Arg Xaa Ile Val 330
 320 325

gtc ccg cct cac ctg ggg tat gga gag gaa gga aga ggg aat atc ccc 1179
 Val Pro Pro His Leu Gly Tyr Gly Glu Glu Gly Arg Gly Asn Ile Pro 350
 335 340 345

ggc tcg gct gtg ctg gtg ttt gac atc cat gtg atc gac ttc cac aac 1227
 Gly Ser Ala Val Leu Val Phe Asp Ile His Val Ile Asp Phe His Asn 365
 355 360

cct tcg gac tcc atc agc atc acc tcc cac tac aaa cct cct gac tgc 1275
 Pro Ser Asp Ser Ile Ser Ile Thr Ser His Tyr Lys Pro Pro Asp Cys 380
 370 375

tca gtg ctg agt aag aag gga gat tac ctc aaa tat cac tac aat gcc 1323
 Ser Val Leu Ser Lys Lys Gly Asp Tyr Leu Lys Tyr His Tyr Asn Ala 395
 385 390

tca ctt ctg gat ggg acc ctg ctg gac tcc acg tgg aat tta ggc aaa 1371
 Ser Leu Leu Asp Gly Thr Leu Leu Asp Ser Thr Trp Asn Leu Gly Lys 410
 400 405

act tac aat att gtt ctg gga tct ggg caa gtt gtg ttg ggg atg gac 1419
 Thr Tyr Asn Ile Val Leu Gly Ser Gly Gln Val Val Leu Gly Met Asp 430
 415 420 425

atg ggt ctc aga gag atg tgc gtt ggc gag aaa cgg aca gtg atc att 1467
 Met Gly Leu Arg Glu Met Cys Val Gly Glu Lys Arg Thr Val Ile Ile 445
 435 440

ccg cct cac ctg ggc tat ggg gaa gct ggc gtg gat gga gaa gtg ccc 1515
 Pro Pro His Leu Gly Tyr Gly Glu Ala Gly Val Asp Gly Glu Val Pro 460
 450 455

ggc agt gcc gta tta gtg ttt gac att gag cts ctg gag ctg gtg gct 1563
 Gly Ser Ala Val Leu Val Phe Asp Ile Glu Xaa Leu Glu Leu Val Ala 475
 465 470

ggc ctt cct gag ggg tac atg ttc ata tgg aat ggt gag gtg tca ccc 1611
 Gly Leu Pro Glu Gly Tyr Met Phe Ile Trp Asn Gly Glu Val Ser Pro 490
 480 485

aac ctc ttt gaa gaa att gac aag gat ggc aac gga gaa gtc ctc ctg 1659
 Asn Leu Phe Glu Glu Ile Asp Lys Asp Gly Asn Gly Glu Val Leu Leu 510
 495 500 505

gaa gag ttc tca gag tac att cac gcc cag gtg gca tct ggc aaa ggg 1707
 Glu Glu Phe Ser Glu Tyr Ile His Ala Gln Val Ala Ser Gly Lys Gly

000502 010649

515

520

525

aaa ctc gct cct ggc ttt gat gct gag ctg att gtg aag aat atg 1752
 Lys Leu Ala Pro Gly Phe Asp Ala Glu Leu Ile Val Lys Asn Met
 530 535 540

ttcaccaacc aggaccggaa tggagatggg aaggtcacag ccgaggaatt taaactcaca 1812
 gaccaggaag ccaaacacga tgtaactcta aacctggcat gaaccagatg gtgcaagggg 1872
 agtacgtgac accaagccac ctgtgtggma agacgtgcar ttgarggtgc aaggggtctc 1932
 tcagaagttt gcatccatta gccagtagta ggtggggcca catagtacct ggtgtacaca 1992
 tcgggggtggg ttgatatatg ggggtgagaag tttgggctga tcgccagtga tagtaaaca 2052
 aatctgtgnc agagggcctt agcatgggat gtgtccagta ttgaccgac gcgtccgcnt 2112
 gccaacatg atttgtgagc cttctgggaa attttgttat taaaggaata tatagtgtnc 2172
 agacggaagt tataatcatc ttggaggaac cataagaaaa ggtgtccagg gtatctatat 2232
 aaagagggtt aaattttttt ttaacttgct ggttaaaaca tttagaaat attctagaga 2292
 tgggcaggag agtcaaaggg cttgcttgcc ccagcagagt tcccagcaga cagccatgga 2352
 tattcccagc agcctgtgca aattctgatg atggcccccac ccccgcacac ggcacacgnc 2412
 acatcawgct tttccagctc atcacacccc gcccantnn gggcctacca ttaatagngt 2472
 atnanttga ggntaaaaga gccttttga cagaaaactg ggccaggnaa aggcattntca 2532
 gaccacaaat agagaatttg attcgtcatt tgccacanaa gtcactgtnt tagcttntcc 2592
 tttccttnan ananatttna nttttttctg gaggcagagt ctccctttgt cgccaggctg 2652
 gagtgcagtg gtgcatctc ggtcactgc agcactgtct cggtcactg cagcktcgc 2712
 ctcccgatc caagcgattc tctgtctca gcctcctgag tagctgggas tacagggtgtg 2772
 caccaccagc cccggctaatt ttttgtttt ttagtagaga cggggtttca ctgtgttggc 2832
 caggatggtc tcaatctga cttcctgatc cgccacactt ggccctccaa agtgttggga 2892
 ttacaggcgt gactcaccat gccagccac ttagttttt cttattcca cttttctatc 2952
 ccatagaaca tcttttttat cttccctgaa ccatatwgat gagataaata gggctggggg 3012
 mtgggcccc ctggctactc aacagagtat ttcccttggc cgagatggaa gttttgtccc 3072
 aatagatgag ctgctgagta tcaacaaggc gacattttt tgctgcccat ttgtgtctg 3132
 gagacggtgg taccctgaag gcagaggcca gtgccgcaag acagcaatga cagtccacct 3192
 gccgacctga ttctgcatc atggaataac cacatggcta cttctatcc tctgttcca 3252
 aatggtggtg gacttatcc tgaagtcgtc aatgacttcc ctttgaaact actttatatt 3312
 actaattdaa actattttgt actgatgtag ccctgaggta gttcatgaaa atgctgtgca 3372
 ctcatccat ggaataaatg ttggaaagct catcttttct gatataaat gttgaatgat 3432

09225502-010699

aaaaaaaaaa aaaaaaaaaa

3451

<210> 6

<211> 541

<212> PRT

<213> Homo sapiens

<400> 6

Met Ala Phe Arg Gly Trp Arg Pro Pro Pro Pro Pro Leu Leu Leu Leu
 1 5 10 15

Leu Leu Trp Val Thr Gly Gln Ala Ala Pro Val Ala Gly Leu Gly Ser
 20 25 30

Asp Ala Glu Leu Gln Ile Glu Arg Arg Phe Val Pro Asp Glu Cys Pro
 35 40 45

Arg Thr Val Arg Ser Gly Asp Phe Val Arg Tyr His Tyr Val Gly Thr
 50 55 60

Phe Pro Asp Gly Gln Lys Phe Asp Ser Ser Tyr Asp Arg Asp Ser Thr
 65 70 75 80

Phe Asn Val Phe Val Gly Lys Gly Gln Leu Ile Thr Gly Met Asp Gln
 85 90 95

Ala Leu Val Gly Met Cys Val Asn Glu Arg Arg Phe Val Lys Ile Pro
 100 105 110

Pro Lys Leu Ala Tyr Gly Asn Glu Arg Val Ser Gly Val Ile Pro Pro
 115 120 125

Asn Ser Val Leu His Phe Asp Val Leu Leu Met Asp Ile Trp Asn Ser
 130 135 140

Glu Asp Gln Val Gln Ile His Thr Tyr Phe Lys Pro Pro Ser Cys Pro
 145 150 155 160

Arg Thr Ile Gln Val Ser Asp Phe Val Arg Tyr His Tyr Asn Gly Thr
 165 170 175

Phe Leu Asp Gly Thr Leu Phe Asp Ser Ser His Asn Arg Met Lys Thr
 180 185 190

Tyr Asp Thr Tyr Val Gly Ile Gly Trp Leu Ile Pro Gly Met Asp Lys
 195 200 205

Gly Leu Leu Gly Met Cys Val Gly Glu Lys Arg Ile Ile Thr Ile Pro
 210 215 220

Pro Phe Leu Ala Tyr Gly Glu Asp Gly Asp Gly Lys Asp Ile Pro Gly
 225 230 235 240

Gln Ala Ser Leu Val Phe Asp Val Ala Leu Leu Asp Leu His Asn Pro
 245 250 255

Lys Asp Ser Ile Ser Ile Glu Asn Lys Val Val Pro Glu Asn Cys Glu
 260 265 270

Arg Ile Ser Gln Ser Gly Asp Phe Leu Thr Tyr His Tyr Asn Gly Thr
 275 280 285

09225502 010699

```
<210> 7
<211> 1251
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (3)..(1166)
```

47

1	5	10	15	
ctg ctg ggg atg tgt gtg ggt gag aag cgc atc atc acc att cct cct	95			
Leu Leu Gly Met Cys Val Gly Glu Lys Arg Ile Ile Thr Ile Pro Pro	20	25	30	
ttt ctg gcc tat gga gag gat gga gat ggg aaa gac att ccc ggt cag	143			
Phe Leu Ala Tyr Gly Glu Asp Gly Asp Gly Lys Asp Ile Pro Gly Gln	35	40	45	
gca tct ctg gtg ttt gat gtt gca tta ttg gac ctc cat aac ccc aag	191			
Ala Ser Leu Val Phe Asp Val Ala Leu Leu Asp Leu His Asn Pro Lys	50	55	60	
gac agc att tcc att gag aac aag gta gta cct gaa aac tgt gag cgg	239			
Asp Ser Ile Ser Ile Glu Asn Lys Val Val Pro Glu Asn Cys Glu Arg	65	70	75	
ata agt caa agt ggg gac ttt ctc agg tat cat tac aat ggc aag ctt	287			
Ile Ser Gln Ser Gly Asp Phe Leu Arg Tyr His Tyr Asn Gly Thr Leu	80	85	90	95
ctg gat ggc acc ctc ttt gat tcc agc tac tct cgg aac cgc acg ttt	335			
Leu Asp Gly Thr Leu Phe Asp Ser Ser Tyr Ser Arg Asn Arg Thr Phe	100	105	110	
gac acg tac att ggg cag ggc tac gtg att cct ggg atg gat gaa ggt	383			
Asp Thr Tyr Ile Gly Gln Gly Tyr Val Ile Pro Gly Met Asp Glu Gly	115	120	125	
cta ctt ggt gtt tgc att gga gaa aag cga agg att gtg gtc ccg cct	431			
Leu Leu Gly Val Cys Ile Gly Glu Lys Arg Arg Ile Val Val Pro Pro	130	135	140	
cac ctg ggg tat gga gag gaa gga aga ggg aat atc ccc ggc tgc gct	479			
His Leu Gly Tyr Gly Glu Glu Gly Arg Gly Asn Ile Pro Gly Ser Ala	145	150	155	
gtg ctg gtg ttt gac atc cat gtg atc gac ttc cac aac cct tgc gac	527			
Val Leu Val Phe Asp Ile His Val Ile Asp Phe His Asn Pro Ser Asp	160	165	170	175
tcc atc agc atc acc tcc gac tac aaa ccc cct gac tgc tca gtg ctg	575			
Ser Ile Ser Ile Thr Ser His Tyr Lys Pro Pro Asp Cys Ser Val Leu	180	185	190	
agt aag aag gga gat tac ctc aaa tat cac tac aat gcc tca ctt ctg	623			
Ser Lys Lys Gly Asp Tyr Leu Lys Tyr His Tyr Asn Ala Ser Leu Leu	195	200	205	
gat ggg acc ctg ctg gac tcc acg tgg aat tta ggc aaa act tac aat	671			
Asp Gly Thr Leu Leu Asp Ser Thr Trp Asn Leu Gly Lys Thr Tyr Asn	210	215	220	
att gtt ctg gga tct ggg caa gtt gtg ttg ggg atg gac atg ggt ctc	719			
Ile Val Leu Gly Ser Gly Gln Val Val Leu Gly Met Asp Met Gly Leu	225	230	235	
aga gag atg tgc gtt ggc gag aaa cgg aca gtg atc att ccg cct cac	767			
Arg Glu Met Cys Val Gly Glu Lys Arg Thr Val Ile Ile Pro Pro His	240	245	250	255

00225502-010699

ctg ggc tat ggg gaa gct ggc gtg gat gga gaa gtg ccc ggc agt gcc 815
 Leu Gly Tyr Gly Glu Ala Gly Val Asp Gly Glu Val Pro Gly Ser Ala
 260 265 270
 gta tta gtg ttt gac att gag ctg ctg gag ctg gtg gct ggc ctt cct 863
 Val Leu Val Phe Asp Ile Glu Leu Leu Glu Leu Val Ala Gly Leu Pro
 275 280 285
 gag ggg tac atg ttc ata tgg aat ggt gag gtg tca ccc aac ctc ttt 911
 Glu Gly Tyr Met Phe Ile Trp Asn Gly Glu Val Ser Pro Asn Leu Phe
 290 295 300
 gaa gaa atc aac aag gtg aca ttt ttc tgc tgc cca ttt gtg tcc tgg 959
 Glu Glu Ile Asn Lys Val Thr Phe Phe Cys Cys Pro Phe Val Ser Trp
 305 310 315
 aga cgg tgg tac cct gaa ggc aga ggc cag ctg ccg caa gac agc aat 1007
 Arg Arg Trp Tyr Pro Glu Gly Arg Gly Gln Leu Pro Gln Asp Ser Asn
 320 325 330 335
 gac agt cca cct gcc gac ctg att cct gca tca tgg aat aac cac atg 1055
 Asp Ser Pro Pro Ala Asp Leu Ile Pro Ala Ser Trp Asn Asn His Met
 340 345 350
 gct acc ttc tat cct ctg ttc cca aat ggt ggt ggc act tat cct gaa 1103
 Ala Thr Phe Tyr Pro Leu Phe Pro Asn Gly Gly Gly Thr Tyr Pro Glu
 355 360 365
 gtc gtc aat gat ttc cct ttg aaa cta ctt tat ttt act aat tta aac 1151
 Val Val Asn Asp Phe Pro Leu Lys Leu Leu Tyr Phe Thr Asn Leu Asn
 370 375 380
 tat ttt gta ctg atg tagccctgag gtagttcatg aaaaatgctg tgcactcatt 1206
 Tyr Phe Val Leu Met
 385
 ccatgggaat aaatgttggg aaagctgaaa aaaaaaaaaa aaaaa 1251

<210> 8

<211> 388

<212> PRT

<213> Homo sapiens

<400> 8

Thr Tyr Gly Glu Ile Gly Trp Leu Ile Pro Gly Met Asp Lys Gly Leu
 1 5 10 15

Leu Gly Met Cys Val Gly Glu Lys Arg Ile Ile Thr Ile Pro Pro Phe
 20 25 30

Leu Ala Tyr Gly Glu Asp Gly Asp Gly Lys Asp Ile Pro Gly Gln Ala
 35 40 45

Ser Leu Val Phe Asp Val Ala Leu Leu Asp Leu His Asn Pro Lys Asp
 50 55 60

Ser Ile Ser Ile Glu Asn Lys Val Val Pro Glu Asn Cys Glu Arg Ile
 65 70 75 80

Ser Gln Ser Gly Asp Phe Leu Arg Tyr His Tyr Asn Gly Thr Leu Leu
 85 90 95

00225502.010599

Asp Gly Thr Leu Phe Asp Ser Ser Tyr Ser Arg Asn Arg Thr Phe Asp
 100 105 110
 Thr Tyr Ile Gly Gln Gly Tyr Val Ile Pro Gly Met Asp Glu Gly Leu
 115 120 125
 Leu Gly Val Cys Ile Gly Glu Lys Arg Arg Ile Val Val Pro Pro His
 130 135 140
 Leu Gly Tyr Gly Glu Glu Gly Arg Gly Asn Ile Pro Gly Ser Ala Val
 145 150 155 160
 Leu Val Phe Asp Ile His Val Ile Asp Phe His Asn Pro Ser Asp Ser
 165 170 175
 Ile Ser Ile Thr Ser His Tyr Lys Pro Pro Asp Cys Ser Val Leu Ser
 180 185 190
 Lys Lys Gly Asp Tyr Leu Lys Tyr His Tyr Asn Ala Ser Leu Leu Asp
 195 200 205
 Gly Thr Leu Leu Asp Ser Thr Trp Asn Leu Gly Lys Thr Tyr Asn Ile
 210 215 220
 Val Leu Gly Ser Gly Gln Val Val Leu Gly Met Asp Met Gly Leu Arg
 225 230 235 240
 Glu Met Cys Val Gly Glu Lys Arg Thr Val Ile Ile Pro Pro His Leu
 245 250 255
 Gly Tyr Gly Glu Ala Gly Val Asp Gly Glu Val Pro Gly Ser Ala Val
 260 265 270
 Leu Val Phe Asp Ile Glu Leu Leu Glu Leu Val Ala Gly Leu Pro Glu
 275 280 285
 Gly Tyr Met Phe Ile Trp Asn Gly Glu Val Ser Pro Asn Leu Phe Glu
 290 295 300
 Glu Ile Asn Lys Val Thr Phe Phe Cys Cys Pro Phe Val Ser Trp Arg
 305 310 315 320
 Arg Trp Tyr Pro Glu Gly Arg Gly Gln Leu Pro Gln Asp Ser Asn Asp
 325 330 335
 Ser Pro Pro Ala Asp Leu Ile Pro Ala Ser Trp Asn Asn His Met Ala
 340 345 350
 Thr Phe Tyr Pro Leu Phe Pro Asn Gly Gly Gly Thr Tyr Pro Glu Val
 355 360 365
 Val Asn Asp Phe Pro Leu Lys Leu Leu Tyr Phe Thr Asn Leu Asn Tyr
 370 375 380
 Phe Val Leu Met
 385

09225503-010699